AMENDMENTS TO THE CLAIMS

This listing of claims replaces all prior versions, and listings, of claims in the present application.

IN THE CLAIMS:

1. (Currently Amended) A method for prognostication of the development of neoplasia and providing guidance for treatment in a human patient having a neoplasia comprising:

a) determining a nucleotide sequence of exons 2-11 of a cancer-related p53 nucleic acid derived from a human neoplastic tissue or body fluid;

b) analyzing the nucleotide sequence determined in step a) for the presence of mutations; and

c) classifying the neoplasia into different subgroups depending on

(i) the presence or absence of a mutation,

and

(ii) whether the patient is node positive or node negative ~~not~~, wherein

the survival rate following adjuvant therapy of node negative patients without a mutation in p53 is not statistically significant, whereas the

survival rate following adjuvant therapy of node negative patients having a mutation in p53 is significantly improved, and

the survival rate following adjuvant therapy of node positive patients without a mutation in p53 is not statistically significant, whereas the survival rate following adjuvant therapy of node positive patients having a mutation in p53 is significantly improved; and

d) prognosticating the development of the neoplasia by combining the results of steps c)(i) and c)(ii), wherein said results are indicative of patient survival and providing guidance for the treatment of the patient.

2. (Currently Amended) The method of claim 1, further comprising the step of typing the mutation of step c) ~~(ii) into a group selected from the group consisting of~~ as a missense mutation, a nonsense mutation, a deletion, or ~~and~~ an insertion.

3. (Currently Amended) A method for prognostication of the development of neoplasia and providing guidance for treatment in a human patient having a neoplasia comprising:

a) determining a nucleotide sequence of exons 2-11 of a cancer-related p53 nucleic acid derived from a human neoplastic tissue or body fluid;

b) analyzing the nucleotide sequence determined in step a) for the presence of mutations; and

c) classifying the neoplasia into different subgroups depending on the presence of a mutation in any of conserved regions I-V of p53 versus the presence of a mutation outside any of the conserved regions I-V of p53,

~~The method of claim 2, further comprising determining the presence, position, and type of mutation and categorizing biological aggressiveness and/or metastatic potential of the neoplasia based upon the presence, position, and type of mutation,~~

~~wherein said neoplasia is breast cancer,~~

~~and~~ wherein a ~~frameshift or nonsense~~ mutation in ~~a~~ conserved region II ~~and~~ or conserved region V of p53 is indicative of poor patient outcome in comparison with a mutation outside the conserved regions I-V of p53, and

~~whereas~~ wherein a ~~missense~~ mutation in ~~a~~ conserved region III ~~and~~ or conserved region IV is indicative of positive patient

outcome in comparison with a mutation outside the conserved regions I-V of p53; and

d) prognosticating the development of the neoplasia by analyzing the results of step c), wherein said results are indicative of patient survival and providing guidance for the treatment of the patient.

4. (Currently Amended) The method of claim 1 or 3, wherein an exon or exons of the sequenced nucleic acid encode a DNA binding domain.

5. (Currently Amended) The method of claim 1 or 3, wherein evolutionary conserved regions of the nucleic acid are analyzed.

6. (Currently Amended) The method of claim 1 or 3, wherein the neoplasia is a breast, lung, prostate, gastric, colorectal, melanoma or leukemia neoplasia.

7. (Previously Presented) The method of claim 6, wherein said neoplasia originates from a breast neoplasia.

8. (Canceled).

9. (Currently Amended) The method of claim ~~8~~ 1 or 3, wherein the adjuvant therapy is radiation or chemotherapy/hormone therapy.

10. (Currently Amended) The method of claim 1 or 3, wherein step a) is carried out using an automated nucleic acid sequencer, computer software optionally being used to (i) track samples and control process steps and/or (ii) to aid in and/or interpret sequence data obtained.

11-15. (Canceled).

16. (New) The method of claim 3, further comprising the step of typing the mutation of step c) as a missense mutation, a nonsense mutation, a deletion, or an insertion.

17. (New) The method of claim 16, wherein a frameshift or nonsense mutation in a conserved region II and/or conserved region V of p53 is indicative of poor patient outcome in

comparison with a mutation outside the conserved regions I-V of p53.

18. (New) The method of claim 16, wherein a missense mutation in a conserved region III and/or conserved region IV is indicative of positive patient outcome in comparison with a mutation outside the conserved regions I-V of p53.

19. (New) The method according to claim 2, wherein the following p53 mutations in a node negative patient are indicative of poor patient outcome:

a Glu→Ala substitution at amino acid position 28;

an Ala→Val substitution at amino acid position 159;

a 9 base pair deletion at amino acid position 177;

a His→Gln substitution at amino acid position 179;

an Arg→His substitution at amino acid position 181;

a nonsense mutation at amino acid position 213;

a Cys→Phe substitution at amino acid position 238;

a Met→Thr substitution at amino acid position 246;

an Arg→Ser substitution at amino acid position 249;

a 9 base pair deletion at amino acid position 267;

an Arg→Gly substitution at amino acid position 280; and

a 2 base pair insertion at amino acid position 340.

20. (New) The method according to claim 2, wherein the following p53 mutations in a node positive patient are indicative of poor patient outcome:

a Pro→Leu substitution at amino acid position 36;

a 200 base pair deletion at amino acid position 120;

a 21 base pair deletion at amino acid position 126;

a nonsense mutation at amino acid position 204;

a Tyr→Cys substitution at amino acid position 205;

a 2 base pair deletion at amino acid position 214;

a His→Arg substitution at amino acid position 214;

a Tyr→Cys substitution at amino acid position 220;

a Met→Ile substitution at amino acid position 237;

an Arg→Gln substitution at amino acid position 248;

an Arg→Trp substitution at amino acid position 248;

a 3 base pair deletion at amino acid position 264;

an Arg→Cys substitution at amino acid position 273;

an Ala→Gly substitution at amino acid position 276;

an Arg→Pro substitution at amino acid position 282;

a Glu→Lys substitution at amino acid position 285; and

a 1 base pair insertion at amino acid position 317.